

#5 RECEIVED  
11/13/01  
1600TECH CENTER 1600/2900  
NOV 09 2001

1636

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/476,202A

DATE: 10/22/2001

TIME: 16:49:09

Input Set : A:\noti.txt

Output Set: N:\CRF3\10222001\I476202A.raw

3 <110> APPLICANT: NOTI, John  
 5 <120> TITLE OF INVENTION: MYELOID CELL PROMOTER AND CONSTRUCTS CONTAINING SAME  
 7 <130> FILE REFERENCE: 052544/0108  
 9 <140> CURRENT APPLICATION NUMBER: US 09/476,202A  
 10 <141> CURRENT FILING DATE: 2000-01-03  
 12 <160> NUMBER OF SEQ ID NOS: 11  
 14 <170> SOFTWARE: PatentIn version 3.0  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 3297  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Homo sapiens  
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 22 <221> NAME/KEY: misc\_feature  
 23 <222> LOCATION: (1641)..(1645)  
 24 <223> OTHER INFORMATION: n can be a, c, g, or t  
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 28 <221> NAME/KEY: CDS  
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60	taacacatgc	taaagggttc	tggttgatg	tggttggtca	cgctgtaat	cccagtactt	180
62	tggtggagg	aggtggagg	attgcttgag	tccaggagct	cgagaccagc	atgggcaaca	240
64	tagtgcgatc	tcgtctctac	aaaaaacaaa	aaaattagct	gggcatgggtg	gtgtgcatca	300
66	gtaatccag	tgactgggag	gctgaggtg	gagaattgct	tgagtctggg	aatttgaggc	360
68	tgacgtgagc	cctgatcatg	ccactgcatt	ccagcatggg	cgacatagca	aaacttgtca	420
70	aaaaaaaaaa	aagtttcttc	tctgccccac	catagacaac	cactcttctg	atttctatct	480
72	tcgtagatga	attttgccca	ttctcttgta	tatgaaagga	accagacatt	aggcattctg	540
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Input Set : A:\noti.txt

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76 cagtttgttc tttgttattt attgtaaaga caggggtctgg ctatgttgcc taggctggtc 660
78 tcgaactgtt ggcctcaagc aatccacctg ccaagctctg ggaccacagg catgagccat 720
80 ggcattctgat ckgtagtttg atcttatttc ttgctgagta gtagcccatg gcatgacttt 780
82 attatttttg gtgtccattc tcctctggag gggctctgct ttttgaaacc acaccctggc 840
84 ctagctcccc ttctccctgc ctctctgcag gctcacatcc acatgccaaag acctctgcag 900
86 ccattctgct tcctgtcctt ccaactcctgt gggacctcag agagctacgg ggctccctgg 960
88 gtaccaactg gctcctgagg cctgggggag ggtgggtctt tgggagaagg aagccaggtc 1020
90 cctgcagggt gtggaggggg acagaatgag ggtttttccc caggatgttg ttggcccctg 1080
92 cccccacttc tgttccataa ttaaccaagc ccctcctacc cactgtgccc ctcttccctg 1140
94 tgtgtggagg ccctgaatca ttattttaac taccocctgg gagggtgagc accttctgtg 1200
96 ctctgtcccc aaccttccac ttccocctcaa cgcgctgctc aggg atg acc ttc ggc 1256
97                                     Met Thr Phe Gly
98                                     1
100 act gtg ctt ctt ctg agt g gtaagtgggg ccagggtgct ggggagaagc 1305
101 Thr Val Leu Leu Leu Ser
102 5 10
104 ttggaggagt tctgagggga ctccatctgg gagggcaggc tgggggctgg tggctggctc 1365
106 caaccactct tatgaggagc tgaggcaggg gagtgttca tgtgcgagtg gcccgagtc 1425
108 agtagagtgt gacctgaatg aagaggggct caggggctgt gctcagggtg cgactaagct 1485
110 acctctccag ctggctatgt tgtcccaggc ttccctgctc ccaactcatg agtccctggt 1545
112 gtgggtgaca gaggtctccc cagcctcccc cgggagtgga aggccacaga agccaccagg 1605
W--> 114 gagggggaaa ggttggacat cacctccctg ggccctnnnnn ttcccccaag tcctgactgc 1665
116 acgtagggaa gagggccctt gctgaaaact gcatcagagt cacattcacg tgccatcaaa 1725
118 aatcaggctt ggctgggtgc ggtggctcat gcttataatc ccagcacttt gggaggccga 1785
120 gatgggcgta tcccctgagg tcaggagttt gtgaccagcc tggccaacat ggtgaaaccc 1845
122 catctttacc aaaaatataa aaattagccg ggcattggtg cgtgcacttg taatcccagc 1905
124 tacttgggaa gctgaggcaa gagaatcgct tgaaccagg agacggaagt tgcagtgagc 1965
126 tgagatcggt ccgttgcaact ccagcctcag caacagagcg agactccatc tcaaaaaaaaa 2025
128 aaaaaaaaaa aagaaaaaaaa agaaaaagag gctgggaggt cctagggatt ggggttctt 2085
130 taactcccag cctccccgcc caccaaatat tcctcag tc ctg gct tct tat cat 2139
131                                     Val Leu Ala Ser Tyr His
132                                     15
134 gga ttc aac ctg gat gtg gag gag cct acg atc ttc cag gag gat gca 2187
135 Gly Phe Asn Leu Asp Val Glu Glu Pro Thr Ile Phe Gln Glu Asp Ala
136 20 25 30
138 ggc ggc ttt ggg cag agc gtg gtg cag ttc ggt gga tct cg 2228
139 Gly Gly Phe Gly Gln Ser Val Val Gln Phe Gly Gly Ser Arg
140 35 40 45
142 gtaggcccc ctcccccaag tgcccgtgc tcccaccct cctgtggctg cagtgcacatg 2288
144 gccatgggtt tgtctccag a ctc gtg gtg gga gca ccc ctg gag gtg gtg 2338
145                                     Leu Val Val Gly Ala Pro Leu Glu Val Val
146                                     50 55
148 gcg gcc aac cag acg gga cgg ctg tat gac tgc gca gct gcc acc ggc 2386
149 Ala Ala Asn Gln Thr Gly Arg Leu Tyr Asp Cys Ala Ala Ala Thr Gly
150 60 65 70
152 atg tgc cag ccc atc ccg ctg cac a gtgagtgacc acctgggaat 2431
153 Met Cys Gln Pro Ile Pro Leu His
154 75 80
156 tgggccccct aacctcctg gacccaactg tgcccccgct tagcttccag tccagacctt 2491

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158 ccccgcaaat gagtgtgtgc tgtgagtgag accccgcgtg tctgcccttg cag tc      2546
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162 cgc cct gag gcc gtg aac atg tcc ttg ggc ctg acc ctg gca gcc tcc      2594
163 Arg Pro Glu Ala Val Asn Met Ser Leu Gly Leu Thr Leu Ala Ala Ser
164          85                      90                      95
166 acc aac ggc tcc cgg ctc ctg gtgagtgagt gtcttggggc acgggggggt      2645
167 Thr Asn Gly Ser Arg Leu Leu
168          100
170 ggggtggggc ggggggtggt gttggggagg aggctggggc tgggagtgaa ggaggagggg      2705
172 ctgctaggga ctccctggctc acaggcttct gcctccag gcc tgt ggc ccg acc ctg      2761
173                                     Ala Cys Gly Pro Thr Leu
174                                     105                                     110
176 cac aga gtc tgt ggg gag aac tca tac tca aag ggt tcc tgc ctc ctg      2809
177 His Arg Val Cys Gly Glu Asn Ser Tyr Ser Lys Gly Ser Cys Leu Leu
178          115                      120                      125
180 ctg ggc tcg cgc tgg gag atc atc cag aca gtc ccc gac gcc acg cca g      2858
181 Leu Gly Ser Arg Trp Glu Ile Ile Gln Thr Val Pro Asp Ala Thr Pro
182          130                      135                      140
184 gtaggtccct ggcaggagct gcaggagggg gttgggcccc cgcagtgcac ctccgattcc      2918
186 tccccattcc cccacag ag   tgt cca cat caa gag atg gac atc gtc ttc      2967
187                               Glu Cys Pro His Gln Glu Met Asp Ile Val Phe
188                               145                               150
190 ctg att gac ggc tct gga agc att gac caa aat gac ttt aac cag atg      3015
191 Leu Ile Asp Gly Ser Gly Ser Ile Asp Gln Asn Asp Phe Asn Gln Met
192          155                      160                      165
194 aag ggc ttt gtc caa gct gtc atg ggc cag ttt gag ggc act gac acc      3063
195 Lys Gly Phe Val Gln Ala Val Met Gly Gln Phe Glu Gly Thr Asp Thr
196 170          175          180          185
198 ctg gtgaagactg ggcaaacaat agtaacaggc actgagccct gggccctccc      3116
199 Leu
202 cactggcctt tgcag ttt gca ctg atg cag tac tca aac ctc ctg aag atc      3167
203                               Phe Ala Leu Met Gln Tyr Ser Asn Leu Leu Lys Ile
204                               190                               195
206 cac ttc acc ttc acc caa ttc cgg acc agc ccg agc cag cag agc ctg      3215
207 His Phe Thr Phe Thr Gln Phe Arg Thr Ser Pro Ser Gln Gln Ser Leu
208          200          205          210
210 gtg gat ccc atc gtc caa ctg aaa ggc ctg acg ttc acg gcc acg ggc      3263
211 Val Asp Pro Ile Val Gln Leu Lys Gly Leu Thr Phe Thr Ala Thr Gly
212 215          220          225          230
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220 <211> LENGTH: 234
221 <212> TYPE: PRT
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224 <220> FEATURE:
225 <221> NAME/KEY: misc_feature
226 <222> LOCATION: (1641)..(1645)
227 <223> OTHER INFORMATION: n can be a, c, g, or t

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236          20          25          30
239 Gly Gly Phe Gly Gln Ser Val Val Gln Phe Gly Gly Ser Arg Leu Val
240          35          40          45
243 Val Gly Ala Pro Leu Glu Val Val Ala Ala Asn Gln Thr Gly Arg Leu
244          50          55          60
247 Tyr Asp Cys Ala Ala Ala Thr Gly Met Cys Gln Pro Ile Pro Leu His
248 65          70          75          80
251 Ile Arg Pro Glu Ala Val Asn Met Ser Leu Gly Leu Thr Leu Ala Ala
252          85          90          95
255 Ser Thr Asn Gly Ser Arg Leu Leu Ala Cys Gly Pro Thr Leu His Arg
256          100         105         110
259 Val Cys Gly Glu Asn Ser Tyr Ser Lys Gly Ser Cys Leu Leu Gly
260          115         120         125
263 Ser Arg Trp Glu Ile Ile Gln Thr Val Pro Asp Ala Thr Pro Glu Cys
264          130         135         140
267 Pro His Gln Glu Met Asp Ile Val Phe Leu Ile Asp Gly Ser Gly Ser
268 145         150         155         160
271 Ile Asp Gln Asn Asp Phe Asn Gln Met Lys Gly Phe Val Gln Ala Val
272          165         170         175
275 Met Gly Gln Phe Glu Gly Thr Asp Thr Leu Phe Ala Leu Met Gln Tyr
276          180         185         190
279 Ser Asn Leu Leu Lys Ile His Phe Thr Phe Thr Gln Phe Arg Thr Ser
280          195         200         205
283 Pro Ser Gln Gln Ser Leu Val Asp Pro Ile Val Gln Leu Lys Gly Leu
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287 Thr Phe Thr Ala Thr Gly Ile Leu Thr Val
288 225         230

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291 &lt;210&gt; SEQ ID NO: 3

292 &lt;211&gt; LENGTH: 21777

293 &lt;212&gt; TYPE: DNA

294 &lt;213&gt; ORGANISM: Homo sapiens

296 &lt;220&gt; FEATURE:

297 &lt;221&gt; NAME/KEY: misc\_feature

298 &lt;222&gt; LOCATION: (1641)..(1645)

299 &lt;223&gt; OTHER INFORMATION: n can be a, c, g, or t

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303 &lt;221&gt; NAME/KEY: misc\_feature

304 &lt;222&gt; LOCATION: (11131)..()

305 &lt;223&gt; OTHER INFORMATION: n can be a, c, g, or t

308 &lt;400&gt; SEQUENCE: 3

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313 ctgtcttttg gagaaaacgt cttgcttggg aaggggcctt tgtcttgtca aggttccaac      180
315 tggaaaccct taggacaggg tccctgctgt gttccccaaa aggacttgac ttcgaatttc      240
317 tacctagaaa tacatggaca atacccccag gcctcagtct ccttctccc atgaggcacg      300

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323	ctccgcctcc	cgggttcaag	taattctgct	gtctcagcct	cctgcgtagc	tgggactaca	480
325	ggcacacgcc	acctcgcccg	gcccgatott	tctaaaatac	agttctgaat	atgctgctca	540
327	tccccacctg	tcttcaacag	ctccccatta	ccctcaggac	aatgtctgaa	ctctccagct	600
329	tcgcgtgaga	agtccccctt	catcccagag	ggtgggcttc	agggcgacac	gcatgagagc	660
331	ctctgtgccc	ccatcacccct	cgtttccagt	gaattagtgt	catgtcagca	tcagctcagg	720
333	gcttcacgtg	ggggctctca	gttccgattc	cccaggctga	attgggagtg	agatgcctgc	780
335	atgctggggt	ctgcacagct	ggcctcccgc	ggttgggtca	acattgctgg	cctggaaggg	840
337	aggagcgccc	tctagggagg	gacatggccc	cgggtcgggt	gcagctcacc	agccccaggg	900
339	gcagaagaga	cccaaccact	tcctatTTTT	tgaggctatg	aatatagtac	ctgaaaaaat	960
341	gccaagcact	agattatTTT	tttaaaaagc	gtacttttaa	tgtttgtgtt	aatacacatt	1020
343	aaaacatgca	caaaaagatg	catctacccg	tcttgggaaa	tatgtcaaag	ggtctaaaaa	1080
345	taaaaaagcc	ttctgtggat	atgagtcctg	aaggatgaca	cccatggggg	ccctttacca	1140
347	cggtyggccc	tggccagcac	tgaggcctgg	ggccaggaca	agaagttaac	cagagttagg	1200
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351	ggctggtgcc	gatggtaagc	tgggtggagct	gtcgggtgga	gggggcatag	aatagagaag	1320
353	ggacaacctc	cagtggctac	ttttccacct	ggaaaggtct	ctggagtgcac	caatactcac	1380
355	aagcgtttcc	tacaagtcct	aggatgtggt	gaagggcaca	ctgtctgcat	atagttagtg	1440
357	attgaagaac	atgttggggg	cccacattga	gagctgctgc	ccacaataag	gtcattcttg	1500
359	ctattatgcc	accatcctgg	cataaagttc	atcatggtgc	ttggcactga	gctggggggc	1560
361	tcacaggaca	agccattcct	gacctcggag	tgacgccact	gcagctatca	ccagcaaggg	1620
363	acccgggccc	tgtggatggt	tcaattagaa	aaacagaagg	gaggcagttg	agtgatttga	1680
365	aggggaagtg	gaaagtggcc	ctttacctcc	agccaaaaat	gtctgtccta	tacatcagca	1740
367	gaggctccaa	aatccctgtg	gattttgaag	cttttgagtc	cccaggatga	ctaattatta	1800
369	tgagtttcc	tcagaaaggg	aatcagaaga	taaggctttg	taagaattca	gccctaattg	1860
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375	aaaattttaa	aattacccag	gcatggtggc	atgtgcttgt	agtcccagct	acttggtagg	2040
377	ctgaagcagg	aggatcactt	gagcctggga	ggttgaggat	acagtgagct	gtgatttggg	2100
379	ccaccacact	ccagcctggg	caacagagaa	agatcatgtc	tcagaaaaaa	aaaaaaaaat	2160
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393	tcccaagtag	ctgggagtac	aggggcgtac	caccatgccc	attttttatt	atttattttt	2580
395	gagacagagt	ctcgtctctg	caccagggct	ggagtgcagt	ggcatgatct	tggctcactg	2640
397	caacctccgc	ctcccagggt	caagttcaag	cgattctcct	gcctcagcct	ctggagtagc	2700
399	tgggattaca	ggcaggcacc	accatttcca	gctaattttt	gtatttttag	tatagatggg	2760
401	gtttcaccat	gttgactagg	ctggtctcga	actcctgacc	tcatgatccg	ccctcctcgg	2820
403	cctccgaaag	tgctgggatt	agaggtatga	gccactgtac	ttggccgaca	aggtgttatt	2880
405	ttctgatatt	cttcccttgg	gtgttattgt	gtacatttgt	tacatttgca	ttttcagggt	2940
407	tggctattgt	gttgcattag	atccccgaat	cacaaaatgg	atcaatggct	caaaagcatg	3000
409	gaagttgtga	ttaaaaacta	atctaattgc	tacaattttac	aataatgtca	tcaaagtcaa	3060
411	tattgacttt	taaatattga	gcccagtgca	cgtatagtat	agacatgcat	accggaataa	3120
413	gtgattgtga	gcaaaaaccc	gaaaatatct	agaaggtatt	atactccctg	acaggtaggt	3180
415	tgtattggtt	ctgacatgta	tttgtcccta	gtgtgctgqc	cattctgaaa	ctttatcaaa	3240

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**

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L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:159 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 1

L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3